

(1) GENERAL INFORMATION:

(i) APPLICANT: Greenspan, Daniel S
Takahara, Kazuhiko
Hoffman, Guy G

(ii) TITLE OF INVENTION: Mammalian Tolloid-Like Protein

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Quarles & Brady
(B) STREET: 1 South Pinckney Street
(C) CITY: Madison
(D) STATE: WI
(E) COUNTRY: US
(F) ZIP: 53703

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0,
Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Berson, Bennett J
(B) REGISTRATION NUMBER: 37094
(C) REFERENCE/DOCKET NUMBER: 960296.93839

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 608-251-5000
(B) TELEFAX: 608-251-9166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide probe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ACGTCCAGAC CGGAGCGGGT GTGGCCCGAT GGGGTCATCC CGTTTGTGAT TGGAGGGAAT 60
TTCACAGGCA GCCAGAGGGC AGTCTTCCGG CAGGCCATGA GACACTGGGA GAAGCATACC 120
TGTGTACACT TCTTGGAGCG CACAGATGAG GACAGCTATA TTGTATTAC CTACCGACCC 180
TGCGGGTGCT GCTCCTACGT GGGTCGCCGA GGTGGGGGCC CCCAGGCCAT CTCCATCGGC 240
AAGAACTGTG ACAAGTTTGG CATCGTGGTC CATGAGCTGG GCCATGTCAT TGGCTTCTGG 300
CAGGAGCACA CGCGGCCCGA CCGCGACCGC 330
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4771 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 611..3652
(D) OTHER INFORMATION: /product= "murine mTll protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACACCCCTT TGCTCTCCGG GCAGTCGGGA GCTTCCCTAG CTTCGGCAGG CTTTAAAGGT 60
CTGGCGGCGT AGAAATGCCT ATCCCCCACC CCCTTCCTCG GTCTCCCCTT TCAGTTCAGA 120
TGTGCTGATG TGCAGACCGG ATTCATCTTC CCCGAGCAGC GGCGGTGGCA GCGGCGGGCG 180
CAGGCGGCTG CAGCTCGCTC TCGGCCGCGG GGTCTTGACA GCGGCGGGGG CGCGGCGCGG 240
GAGCCGGAGC TCCGGTGGCA GCTGAGCCCG CCGTGCGCCT CTCGCCGCGG CCGGTCGTGA 300
TCGCGGGAAG TTCGACCGCT GGAAGGACGA CCTAGACCGA GCCGGGTGGT CTGCGGCTGC 360
CCTGCGCCGA GCTCCTCACC TGCCTTCCGC CCACCCGCGG GCGGCGGGCC AAGTTCCCCA 420
GCATCCGGGG GAGACAGGGA GACATTTGCC CTCTCTAGCG TCCTGAAGAC ATCCGCATGT 480
CTCCGGACAC CTGAACATTC AGGTCTTTCC GAGGAGCTTC CCAGTCGGGA TAAGAACACT 540
GTCCCTAGAG CCCCGCATAT CCACGCGGCC CTCCGGGTCT GGTCCCCTCC TTTTCTCTA 600
GGGGAGGAGG ATG GGT TTG CAA GCG CTC TCC CCG AGG ATG CTC CTG TGG 649
Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp
1 5 10
TTG GTG GTC TCG GGT ATT GTT TTC TCC CGG GTG CTG TGG GTC TGC GCT 697
Leu Val Val Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala
15 20 25
GGC CTC GAT TAT GAT TAC ACT TTT GAT GGG AAC GAA GAG GAC AAA ACG 745
Gly Leu Asp Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr
30 35 40 45
GAG CCT ATA GAT TAC AAG GAC CCG TGC AAA GCT GCT GTG TTT TGG GGT 793
Glu Pro Ile Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly
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GAC ATC GCC TTA GAT GAT GAA GAC TTA AAT ATC TTC CAA ATA GAC AGG 841
Asp Ile Ala Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg
65 70 75
ACA ATT GAC CTG ACC CAG AGC CCC TTT GGA AAA CTT GGA CAT ATT ACA 889
Thr Ile Asp Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr
80 85 90
GGT GGC TTT GGA GAC CAT GGC ATG CCA AAG AAG CGA GGG GCA CTC TAC 937
Gly Gly Phe Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr
95 100 105

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	Gln	Leu	Ile	Glu	Arg	Ile	Arg	Arg	Ile	Gly	Ser	Gly	Leu	Glu	Gln	Asn	
	110					115				120					125		
5	AAC	ACG	ATG	AAG	GGA	AAA	GCA	CCT	CCA	AAA	TTG	TCA	GAG	CAA	AGT	GAG	1033
	Asn	Thr	Met	Lys	Gly	Lys	Ala	Pro	Pro	Lys	Leu	Ser	Glu	Gln	Ser	Glu	
					130					135					140		
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10	CCT	GGG	GGT	GTC	ATT	CCT	TAT	GTC	ATA	GGA	GGA	AAC	TTT	ACT	GGC	AGC	1129
	Pro	Gly	Gly	Val	Ile	Pro	Tyr	Val	Ile	Gly	Gly	Asn	Phe	Thr	Gly	Ser	
				160				165					170				
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				175			180					185					
	TGT	GTG	ACG	TTC	ACT	GAG	AGA	AGT	GAT	GAA	GAA	AGT	TAT	ATT	GTG	TTC	1225
	Cys	Val	Thr	Phe	Thr	Glu	Arg	Ser	Asp	Glu	Glu	Ser	Tyr	Ile	Val	Phe	
	190					195				200					205		
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					210					215					220		
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	Gly	Pro	Gln	Ala	Ile	Ser	Ile	Gly	Lys	Asn	Cys	Asp	Lys	Phe	Gly	Ile	
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30	Arg	Pro	Asp	Arg	Asp	Asn	His	Val	Thr	Ile	Ile	Arg	Glu	Asn	Ile	Gln	
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	CCA	GGT	CAA	GAG	TAC	AAT	TTT	CTA	AAG	ATG	GAG	CCT	GGA	GAA	GTG	AAC	1465
	Pro	Gly	Gln	Glu	Tyr	Asn	Phe	Leu	Lys	Met	Glu	Pro	Gly	Glu	Val	Asn	
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	TCT	CTT	GGG	GAA	AGA	TAT	GAT	TTT	GAC	AGT	ATC	ATG	CAC	TAC	GCC	AGG	1513
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	Asn	Thr	Phe	Ser	Arg	Gly	Met	Phe	Leu	Asp	Thr	Ile	Leu	Pro	Ser	Arg	
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	GAT	GAT	AAT	GGC	ATT	CGT	CCT	GCA	ATT	GGT	CAA	CGG	ACC	CGG	TTA	AGC	1609
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	Gly	Glu	Thr	Leu	Gln	Glu	Ser	Ser	Gly	Asn	Leu	Ser	Ser	Pro	Gly	Phe	
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	CCA	AAT	GGC	TAC	CCT	TCC	TAC	ACA	CAC	TGC	ATC	TGG	AGA	GTG	TCT	GTG	1753
50	Pro	Asn	Gly	Tyr	Pro	Ser	Tyr	Thr	His	Cys	Ile	Trp	Arg	Val	Ser	Val	
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5	AAA	AGT	AGT	TTG	TGC	TGG	TAT	GAT	TAC	ATT	GAA	GTA	AGA	GAT	GGT	TAC	1849
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			400					405					410				
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	Trp	Arg	Lys	Ser	Pro	Leu	Leu	Gly	Arg	Phe	Cys	Gly	Asp	Lys	Val	Ala	
		415					420					425					
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	AGC	AGT	AAC	TGG	GTA	GGA	AAA	GGG	TTT	GCA	GCT	GTC	TAT	GAA	GCG	ATT	1993
	Ser	Ser	Asn	Trp	Val	Gly	Lys	Gly	Phe	Ala	Ala	Val	Tyr	Glu	Ala	Ile	
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				465					470					475			
	TAC	CCC	GAT	GAC	TAC	CGA	CCA	ATG	AAG	GAG	TGT	GTA	TGG	AAA	ATA	ATG	2089
	Tyr	Pro	Asp	Asp	Tyr	Arg	Pro	Met	Lys	Glu	Cys	Val	Trp	Lys	Ile	Met	
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	Ala	Ser	Glu	Asn	Ser	Pro	Leu	Ile	Gly	Arg	Phe	Cys	Gly	Tyr	Asp	Lys	
					530					535					540		
	CCT	GAA	GAT	ATA	AGG	TCT	ACT	TCC	AAC	ACC	CTG	TGG	ATG	AAG	TTT	GTC	2281
	Pro	Glu	Asp	Ile	Arg	Ser	Thr	Ser	Asn	Thr	Leu	Trp	Met	Lys	Phe	Val	
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35	TCT	GAC	GGG	ACT	GTG	AAC	AAG	GCA	GGG	TTT	GCT	GCG	AAC	TTT	TTT	AAA	2329
	Ser	Asp	Gly	Thr	Val	Asn	Lys	Ala	Gly	Phe	Ala	Ala	Asn	Phe	Phe	Lys	
				560				565					570				
	GAG	GAA	GAT	GAG	TGT	GCC	AAA	CCT	GAC	CGA	GGA	GGC	TGT	GAA	CAG	AGG	2377
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	Cys	Leu	Asn	Thr	Leu	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	
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45					610					615					620		
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	Tyr	Pro	Pro	Asn	Lys	Asn	Cys	Val	Trp	Gln	Val	Ile	Ala	Pro	Ser	Gln	
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		TAC	AGA	ATC	TCT	GTG	AAG	TTT	GAG	TTT	TTT	GAA	TTG	GAA	GGC	AAT	GAA	2617
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5		GTT	TGC	AAA	TAC	GAT	TAC	GTG	GAG	ATC	TGG	AGC	GGC	CCT	TCC	TCT	GAG	2665
		Val	Cys	Lys	Tyr	Asp	Tyr	Val	Glu	Ile	Trp	Ser	Gly	Pro	Ser	Ser	Glu	
			670				675					680					685	
		TCT	AAA	CTG	CAT	GGC	AAG	TTC	TGT	GGC	GCT	GAC	ATA	CCT	GAA	GTG	ATG	2713
		Ser	Lys	Leu	His		Lys	Phe	Cys	Gly	Ala	Asp	Ile	Pro	Glu	Val	Met	
					690						695					700		
10		ACT	TCC	CAT	TTC	AAC	AAC	ATG	AGG	ATT	GAA	TTC	AAG	TCA	GAC	AAC	ACT	2761
		Thr	Ser	His	Phe	Asn	Asn	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	
					705					710					715			
		GTA	TCC	AAG	AAG	GGC	TTC	AAA	GCA	CAT	TTT	TTC	TCA	GAT	AAG	GAT	GAG	2809
15		Val	Ser	Lys	Lys	Gly	Phe	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	
				720					725					730				
		TGT	TCA	AAG	GAT	AAT	GGT	GGC	TGT	CAG	CAT	GAG	TGT	GTC	AAC	ACG	ATG	2857
		Cys	Ser	Lys	Asp	Asn	Gly	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	
				735			740						745					
		GGA	AGT	TAC	ACG	TGT	CAG	TGC	CGG	AAT	GGA	TTC	GTG	TTG	CAT	GAG	AAC	2905
20		Gly	Ser	Tyr	Thr	Cys	Gln	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Glu	Asn	
						755						760					765	
		AAG	CAT	GAT	TGC	AAG	GAA	GCC	GAG	TGT	GAA	CAG	AAG	ATA	CAC	AGC	CCA	2953
		Lys	His	Asp	Cys	Lys	Glu	Ala	Glu	Cys	Glu	Gln	Lys	Ile	His	Ser	Pro	
						770					775					780		
25		AGT	GGT	CTC	ATC	ACC	AGT	CCC	AAC	TGG	CCA	GAC	AAG	TAT	CCA	AGC	AGG	3001
		Ser	Gly	Leu	Ile	Thr	Ser	Pro	Asn	Trp	Pro	Asp	Lys	Tyr	Pro	Ser	Arg	
					785					790					795			
		AAA	GAG	TGC	ACG	TGG	GTG	ATC	AGT	GCC	ATT	CCT	GGC	CAC	CGC	ATC	ACA	3049
30		Lys	Glu	Cys	Thr	Trp	Val	Ile	Ser	Ala	Ile	Pro	Gly	His	Arg	Ile	Thr	
				800					805					810				
		TTA	GCC	TTC	AAT	GAG	TTT	GAG	GTT	GAA	CAA	CAT	CAA	GAA	TGT	GCT	TAT	3097
		Leu	Ala	Phe	Asn	Glu	Phe	Glu	Val	Glu	Gln	His	Gln	Glu	Cys	Ala	Tyr	
				815				820					825					
		GAT	CAC	TTG	GAA	ATT	TTT	GAT	GGA	GAA	ACG	GAG	AAG	TCA	CCA	ATA	CTT	3145
35		Asp	His	Leu	Glu	Ile	Phe	Asp	Gly	Glu	Thr	Glu	Lys	Ser	Pro	Ile	Leu	
						835						840					845	
		GGC	CGA	CTA	TGT	GGC	AGC	AAG	ATA	CCA	GAT	CCC	CTC	ATG	GCT	ACT	GGG	3193
		Gly	Arg	Leu	Cys	Gly	Ser	Lys	Ile	Pro	Asp	Pro	Leu	Met	Ala	Thr	Gly	
						850					855					860		
40		AAT	GAA	ATG	TTT	ATT	CGG	TTT	ATT	TCT	GAT	GCC	TCT	GTT	CAA	AGA	AAA	3241
		Asn	Glu	Met	Phe	Ile	Arg	Phe	Ile	Ser	Asp	Ala	Ser	Val	Gln	Arg	Lys	
					865					870					875			
		GGC	TTT	CAA	GCT	ACA	CAT	TCC	ACA	GAG	TGT	GGT	GGT	CGA	TTG	AAA	GCA	3289
45		Gly	Phe	Gln	Ala	Thr	His	Ser	Thr	Glu	Cys	Gly	Gly	Arg	Leu	Lys	Ala	
				880						885				890				
		GAG	TCA	AAG	CCT	AGA	GAC	CTG	TAC	TCC	CAT	GCT	CAG	TTT	GGT	GAT	AAT	3337
		Glu	Ser	Lys	Pro	Arg	Asp	Leu	Tyr	Ser	His	Ala	Gln	Phe	Gly	Asp	Asn	
				895				900					905					
50		AAC	TAC	CCA	GGA	CAA	CTG	GAC	TGT	GAA	TGG	TTG	TTG	GTG	TCA	GAA	CGA	3385
		Asn	Tyr	Pro	Gly	Gln	Leu	Asp	Cys	Glu	Trp	Leu	Leu	Val	Ser	Glu	Arg	
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	GGA TCT CGA CTT GAA TTG TCC TTC CAG ACA TTC GAA GTA GAA GAA GAA	3433
	Gly Ser Arg Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Glu	
	930 935 940	
5	GCT GAC TGT GGC TAT GAC TAT GTT GAA GTC TTT GAT GGT CTC AGT TCA	3481
	Ala Asp Cys Gly Tyr Asp Tyr Val Glu Val Phe Asp Gly Leu Ser Ser	
	945 950 955	
	AAA GCT GTG GGT CTT GGT AGA TTC TGT GGG TCA GGG CCA CCA GAA GAA	3529
	Lys Ala Val Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu	
	960 965 970	
10	ATC TAT TCA ATT GGA GAT GTG GCT TTG ATT CAT TTC CAC ACA GAT GAC	3577
	Ile Tyr Ser Ile Gly Asp Val Ala Leu Ile His Phe His Thr Asp Asp	
	975 980 985	
	ACT ATC AAC AAG AAA GGA TTT TAT ATA AGA TAT AAA AGT ATA AGA TAC	3625
	Thr Ile Asn Lys Lys Gly Phe Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr	
15	990 995 1000 1005	
	CCG GAA ACG ATG CAT GCC AAG AAC TAA TGCCGACCCT CCCTCAGAAC	3672
	Pro Glu Thr Met His Ala Lys Asn *	
	1010	
	AGAAAGGAAT GTGCATATGG AAAGAAGACA TTTTAAAAAT AGACAATATT AATACAATTG	3732
20	TTTTATATAA TGAATTTGAG CAAAAGAAAC CTGCAAGATT AGAGTTATCT CTGAAGTGAA	3792
	AGAGAACTTT CCAGAAAACC TGATTGGCAT TGCAAGGATG TTTGAAAGTC ATGCTTGTTC	3852
	AAGGAAGATT AACAGCTTGA AATAGATGCT TCACATTTTG GACAGTTCAT TTAATGAGCT	3912
	GTGATTCTCT GGAGTGATTT CTTGACTACT TTTCCAAGAT CTGGGGACGT AGAAATGATG	3972
	GGACGGATCA TAGCTTGGA ACCCACTTCT TGGGTCTTAG CATGTTTGCT TAGACTCTGT	4032
	AGGTCAGACA CAGTGTA AAC CAAATTCATG TAAGGTGATG TGGAATAGTG GTCTTTGGAA	4092
	GGTGGTTCAT CATTTAAATG TAGGTTTGTG CTTGTGTGTA TGTTACATA TGCAAGTGTG	4152
	TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGCGTG TGTGTGTGTG TGC GTGTGTG	4212
	TGTGTGTGCA TGTGTGTGCA TGTGTGTTTG GAAACTGGAA TATTTTCATCT TCATTATTTT	4272
	CAAATGCAGG CCAGCTTAAC CTGTTACAC AAATGATTTT GTGACCACTT CATTGTATCT	4332
30	GTATCTTGAG AAGTTTGAAA TATCTATAGT GTCTACAATG CAGTTAATCC CTAGATATCG	4392
	GATAATACCC AGTTCAC TAG TAAACTCATT TCTCTCTGGG GAAGTGCTGA ATAGTCTCCA	4452
	AATTCAAGAA ACTCACCATG TCTTATAAAC CTTTAAGATA AAATTCCAAC GAGGTGTGTG	4512
	CAGCCATCTT CCAAATGACT GCCTGGATGT TTCTTAGTCC AGTTACTACT GCTGCTGCTA	4572
	TTGGTCTTTC TTTTATTGTT AATGTGTTGA TATGTTGTTA TTATTATGGT TATTATTATT	4632
35	GATGTTGTTA CTATATTTAA AAATGATGAG ATGAAGTGGA AGTAGAGTTT GGGAGAAATG	4692
	AAATCTCTCT TTTTGTCT CTTCTTGAAA TTCAGTTTCA AAAAATACAA TATTGGGTGG	4752
	CAAAAAAAAA AAAAAAAAAA	4771

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp Leu Val Val
1 5 10 15
Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala Gly Leu Asp
20 25 30
Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Pro Ile
35 40 45
Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala
50 55 60
Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg Thr Ile Asp
65 70 75 80
Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr Gly Gly Phe
85 90 95
Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr Gln Leu Ile
100 105 110
Glu Arg Ile Arg Arg Ile Gly Ser Gly Leu Glu Gln Asn Asn Thr Met
115 120 125
Lys Gly Lys Ala Pro Pro Lys Leu Ser Glu Gln Ser Glu Lys Asn Arg
130 135 140
Val Pro Arg Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp Pro Gly Gly
145 150 155 160
Val Ile Pro Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln Arg Ala
165 170 175
Met Phe Lys Gln Ala Met Arg His Trp Glu Lys His Thr Cys Val Thr
180 185 190
Phe Thr Glu Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe Thr Tyr Arg
195 200 205
Pro Cys Gly Cys Cys Ser Tyr Val Gly Arg Arg Gly Asn Gly Pro Gln
210 215 220
Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile Val Val His
225 230 235 240
Glu Leu Gly His Val Ile Gly Phe Trp His Glu His Thr Arg Pro Asp
245 250 255
Arg Asp Asn His Val Thr Ile Ile Arg Glu Asn Ile Gln Pro Gly Gln
260 265 270
Glu Tyr Asn Phe Leu Lys Met Glu Pro Gly Glu Val Asn Ser Leu Gly
275 280 285
Glu Arg Tyr Asp Phe Asp Ser Ile Met His Tyr Ala Arg Asn Thr Phe
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Ser 305	Arg	Gly	Met	Phe	Leu 310	Asp	Thr	Ile	Leu	Pro 315	Ser	Arg	Asp	Asp	Asn 320
Gly	Ile	Arg	Pro	Ala 325	Ile	Gly	Gln	Arg	Thr 330	Arg	Leu	Ser	Lys	Gly 335	Asp
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Leu	Gln	Glu 355	Ser	Ser	Gly	Asn	Leu 360	Ser	Ser	Pro	Gly	Phe 365	Pro	Asn	Gly
Tyr	Pro 370	Ser	Tyr	Thr	His	Cys 375	Ile	Trp	Arg	Val	Ser 380	Val	Thr	Pro	Gly
Glu 385	Lys	Ile	Val	Leu	Asn 390	Phe	Thr	Thr	Met	Asp 395	Leu	Tyr	Lys	Ser	Ser 400
Leu	Cys	Trp	Tyr	Asp 405	Tyr	Ile	Glu	Val	Arg 410	Asp	Gly	Tyr	Trp	Arg 415	Lys
Ser	Pro	Leu 420	Leu	Gly	Arg	Phe	Cys	Gly 425	Asp	Lys	Val	Ala	Gly 430	Val	Leu
Thr	Ser	Thr 435	Asp	Ser	Arg	Met	Trp 440	Ile	Glu	Phe	Arg	Ser 445	Ser	Ser	Asn
Trp	Val 450	Gly	Lys	Gly	Phe	Ala 455	Ala	Val	Tyr	Glu	Ala 460	Ile	Cys	Gly	Gly
Glu 465	Ile	Arg	Lys	Asn 470	Glu	Gly	Gln	Ile	Gln	Ser 475	Pro	Asn	Tyr	Pro	Asp 480
Asp	Tyr	Arg	Pro	Met 485	Lys	Glu	Cys	Val	Trp 490	Lys	Ile	Met	Val	Ser 495	Glu
Gly	Tyr	His 500	Val	Gly	Leu	Thr	Phe	Gln 505	Ala	Phe	Glu	Ile	Glu 510	Arg	His
Asp	Ser	Cys 515	Ala	Tyr	Asp	His	Leu 520	Glu	Val	Arg	Asp	Gly 525	Ala	Ser	Glu
Asn	Ser 530	Pro	Leu	Ile	Gly	Arg 535	Phe	Cys	Gly	Tyr	Asp 540	Lys	Pro	Glu	Asp
Ile 545	Arg	Ser	Thr	Ser	Asn 550	Thr	Leu	Trp	Met	Lys 555	Phe	Val	Ser	Asp	Gly 560
Thr	Val	Asn	Lys	Ala 565	Gly	Phe	Ala	Ala	Asn 570	Phe	Phe	Lys	Glu	Glu 575	Asp
Glu	Cys	Ala	Lys 580	Pro	Asp	Arg	Gly	Gly 585	Cys	Glu	Gln	Arg	Cys 590	Leu	Asn
Thr	Leu	Gly 595	Ser	Tyr	Gln	Cys	Ala 600	Cys	Glu	Pro	Gly	Tyr 605	Glu	Leu	Gly
Pro 610	Asp	Arg	Arg	Ser	Cys	Glu 615	Ala	Ala	Cys	Gly	Gly 620	Leu	Leu	Thr	Lys
Leu 625	Asn	Gly	Thr	Ile	Thr 630	Thr	Pro	Gly	Trp	Pro 635	Lys	Glu	Tyr	Pro	Pro 640
Asn	Lys	Asn	Cys 645	Val	Trp	Gln	Val	Ile	Ala 650	Pro	Ser	Gln	Tyr	Arg 655	Ile

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	Ser	Val	Lys	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	Val	Cys	Lys	
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			675					680					685				
5	His	Gly	Lys	Phe	Cys	Gly	Ala	Asp	Ile	Pro	Glu	Val	Met	Thr	Ser	His	
		690					695					700					
	Phe	Asn	Asn	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	Val	Ser	Lys	
	705					710					715					720	
10	Lys	Gly	Phe	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	Cys	Ser	Lys	
					725					730					735		
	Asp	Asn	Gly	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	Gly	Ser	Tyr	
				740					745					750			
	Thr	Cys	Gln	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Glu	Asn	Lys	His	Asp	
			755					760					765				
15	Cys	Lys	Glu	Ala	Glu	Cys	Glu	Gln	Lys	Ile	His	Ser	Pro	Ser	Gly	Leu	
	770						775					780					
	Ile	Thr	Ser	Pro	Asn	Trp	Pro	Asp	Lys	Tyr	Pro	Ser	Arg	Lys	Glu	Cys	
	785					790					795					800	
20	Thr	Trp	Val	Ile	Ser	Ala	Ile	Pro	Gly	His	Arg	Ile	Thr	Leu	Ala	Phe	
					805					810					815		
	Asn	Glu	Phe	Glu	Val	Glu	Gln	His	Gln	Glu	Cys	Ala	Tyr	Asp	His	Leu	
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	Glu	Ile	Phe	Asp	Gly	Glu	Thr	Glu	Lys	Ser	Pro	Ile	Leu	Gly	Arg	Leu	
				835				840					845				
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	850						855					860					
	Phe	Ile	Arg	Phe	Ile	Ser	Asp	Ala	Ser	Val	Gln	Arg	Lys	Gly	Phe	Gln	
	865					870					875					880	
30	Ala	Thr	His	Ser	Thr	Glu	Cys	Gly	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Lys	
					885					890					895		
	Pro	Arg	Asp	Leu	Tyr	Ser	His	Ala	Gln	Phe	Gly	Asp	Asn	Asn	Tyr	Pro	
				900					905					910			
	Gly	Gln	Leu	Asp	Cys	Glu	Trp	Leu	Leu	Val	Ser	Glu	Arg	Gly	Ser	Arg	
			915					920					925				
35	Leu	Glu	Leu	Ser	Phe	Gln	Thr	Phe	Glu	Val	Glu	Glu	Glu	Ala	Asp	Cys	
	930						935					940					
	Gly	Tyr	Asp	Tyr	Val	Glu	Val	Phe	Asp	Gly	Leu	Ser	Ser	Lys	Ala	Val	
	945					950					955					960	
40	Gly	Leu	Gly	Arg	Phe	Cys	Gly	Ser	Gly	Pro	Pro	Glu	Glu	Ile	Tyr	Ser	
					965					970					975		
	Ile	Gly	Asp	Val	Ala	Leu	Ile	His	Phe	His	Thr	Asp	Asp	Thr	Ile	Asn	
				980					985					990			
	Lys	Lys	Gly	Phe	Tyr	Ile	Arg	Tyr	Lys	Ser	Ile	Arg	Tyr	Pro	Glu	Thr	
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Met His Ala Lys Asn *
1010

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 648..3689
- (D) OTHER INFORMATION: /product= "human mTll protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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GTGCTGATGT GCAGACCGGA TTCATCTTCT CGGAGCTGCG GCGGCGGCTT TGGGCTCAGG 180
CGGCGGCGGC TCGCGCTCGG CCGCGGAGTC CTGGCAGCAG CGGGGACGCG GCGCGGGAGT 240
CCGAGCTCTG GTGGCAGCTG AGCCCGCGGG GCGCCGCTCG CCGAGCCGCG GCCCGGGGAA 300
GTTCCGGCAGC CAGAAGGACG ACCTGGCAGG CTGCGAGCGC CAGCGCCGCC AGAGCCGAGT 360
TTGCTTGCGC CCTCCCCGCC TCCGAGTGCA GAGTTCCTTA CCTGCCCTCC GCCCACCCGT 420
GGGCCCCTAG CCAACTTCTC CCTGCGACTG GGGGTAACAG GCAGTGCTTG CCCTCTCTAC 480
TGTCCCGGCG GCATCCACAT GTTTCGGAC ACCTGAGCAC CCCGGTCCCG CCGAGGAGCC 540
TCCGGGTGGG GAGAAGAGCA CCGGTGCCCC TAGCCCCGCA CATCAGCGCG GACCGCGGCT 600
GCCTAACCTC TGGGTCCCGT CCCCTCCTTT TCCTCCGGGG GAGGAGG ATG GGG TTG 656
                                         Met Gly Leu
                                         1015
GGA ACG CTT TCC CCG AGG ATG CTC GTG TGG CTG GTG GCC TCG GGG ATT 704
Gly Thr Leu Ser Pro Arg Met Leu Val Trp Leu Val Ala Ser Gly Ile
      1020                      1025                      1030
GTT TTC TAC GGG GAG CTA TGG GTC TGC GCT GGC CTC GAT TAT GAT TAC 752
Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly Leu Asp Tyr Asp Tyr
      1035                      1040                      1045
ACT TTT GAT GGG AAC GAA GAG GAT AAA ACA GAG ACT ATA GAT TAC AAG 800
Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Thr Ile Asp Tyr Lys
      1050                      1055                      1060                      1065
GAC CCG TGT AAA GCC GCT GTA TTT TGG GGC GAT ATT GCC TTA GAT GAT 848
Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala Leu Asp Asp
      1070                      1075                      1080
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50

004436-065
105220-994660

	GCA AGA AAG CTG TAT AGA TGT CCA GCA TGT GGA GAA ACT CTA CAA GAA	1712
	Ala Arg Lys Leu Tyr Arg Cys Pro Ala Cys Gly Glu Thr Leu Gln Glu	
	1355 1360 1365	
5	TCC AAT GGC AAC CTT TCC TCT CCA GGA TTT CCC AAT GGC TAC CCT TCT	1760
	Ser Asn Gly Asn Leu Ser Ser Pro Gly Phe Pro Asn Gly Tyr Pro Ser	
	1370 1375 1380 1385	
	TAC ACA CAC TGC ATC TGG AGA GTT TCT GTG ACC CCA GGG GAG AAG ATT	1808
	Tyr Thr His Cys Ile Trp Arg Val Ser Val Thr Pro Gly Glu Lys Ile	
	1390 1395 1400	
10	GTT TTA AAT TTT ACA ACG ATG GAT CTA TAC AAG AGT AGT TTG TGC TGG	1856
	Val Leu Asn Phe Thr Thr Met Asp Leu Tyr Lys Ser Ser Leu Cys Trp	
	1405 1410 1415	
	TAT GAC TAT ATT GAA GTA AGA GAC GGG TAC TGG AGA AAA TCA CCT CTC	1904
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	Leu Gly Arg Phe Cys Gly Asp Lys Leu Pro Glu Val Leu Thr Ser Thr	
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	Asp Ser Arg Met Trp Ile Glu Phe Arg Ser Ser Ser Asn Trp Val Gly	
	1450 1455 1460 1465	
	AAA GGC TTT GCA GCT GTC TAT GAA GCG ATC TGT GGA GGT GAG ATA CGT	2048
	Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile Cys Gly Gly Glu Ile Arg	
	1470 1475 1480	
25	AAA AAT GAA GGA CAG ATT CAG TCT CCC AAT TAT CCT GAT GAC TAT CGC	2096
	Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn Tyr Pro Asp Asp Tyr Arg	
	1485 1490 1495	
	CCG ATG AAA GAA TGT GTG TGG AAA ATA ACA GTG TCT GAG AGC TAC CAC	2144
	Pro Met Lys Glu Cys Val Trp Lys Ile Thr Val Ser Glu Ser Tyr His	
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	Val Gly Leu Thr Phe Gln Ser Phe Glu Ile Glu Arg His Asp Asn Cys	
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	Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly Thr Ser Glu Asn Ser Pro	
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	TTG ATA GGG CGT TTC TGT GGT TAT GAC AAA CCT GAA GAC ATA AGA TCT	2288
	Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys Pro Glu Asp Ile Arg Ser	
	1550 1555 1560	
40	ACC TCC AAT ACT TTG TGG ATG AAG TTT GTT TCT GAC GGA ACT GTG AAC	2336
	Thr Ser Asn Thr Leu Trp Met Lys Phe Val Ser Asp Gly Thr Val Asn	
	1565 1570 1575	
	AAA GCA GGG TTT GCT GCT AAC TTT TTT AAA GAG GAA GAT GAG TGT GCC	2384
	Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys Glu Glu Asp Glu Cys Ala	
	1580 1585 1590	
45	AAA CCT GAC CGT GGA GGC TGT GAG CAG CGA TGT CTG AAC ACT CTG GGC	2432
	Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg Cys Leu Asn Thr Leu Gly	
	1595 1600 1605	
50	AGT TAC CAG TGT GCC TGT GAG CCT GGC TAT GAG CTG GGC CCA GAC AGA	2480
	Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr Glu Leu Gly Pro Asp Arg	
	1610 1615 1620 1625	

0092366
162300
T62300

	AGG	AGC	TGT	GAA	GCT	GCT	TGT	GGT	GGA	CTT	CTT	ACC	AAA	CTT	AAC	GGC	2528
	Arg	Ser	Cys	Glu	Ala	Ala	Cys	Gly	Gly	Leu	Leu	Thr	Lys	Leu	Asn	Gly	
				1630						1635					1640		
5	ACC	ATA	ACC	ACC	CCT	GGC	TGG	CCC	AAG	GAG	TAC	CCT	CCT	AAT	AAG	AAC	2576
	Thr	Ile	Thr	Thr	Pro	Gly	Trp	Pro	Lys	Glu	Tyr	Pro	Pro	Asn	Lys	Asn	
				1645					1650					1655			
	TGT	GTG	TGG	CAA	GTG	GTT	GCA	CCA	ACC	CAG	TAC	AGA	ATT	TCT	GTG	AAG	2624
	Cys	Val	Trp	Gln	Val	Val	Ala	Pro	Thr	Gln	Tyr	Arg	Ile	Ser	Val	Lys	
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	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	Val	Cys	Lys	Tyr	Asp	Tyr	
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	GTG	GAG	ATC	TGG	AGT	GGT	CTT	TCC	TCT	GAG	TCT	AAA	CTG	CAT	GGC	AAA	2720
15	Val	Glu	Ile	Trp	Ser	Gly	Leu	Ser	Ser	Glu	Ser	Lys	Leu	His	Gly	Lys	
		1690					1695					1700				1705	
	TTC	TGT	GGC	GCT	GAA	GTG	CCT	GAA	GTG	ATC	ACA	TCC	CAG	TTC	AAC	AAT	2768
	Phe	Cys	Gly	Ala	Glu	Val	Pro	Glu	Val	Ile	Thr	Ser	Gln	Phe	Asn	Asn	
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	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	Val	Ser	Lys	Lys	Gly	Phe	
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	AAA	GCA	CAT	TTT	TTC	TCA	GAC	AAA	GAT	GAA	TGC	TCT	AAG	GAT	AAT	GGT	2864
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	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	Gly	Ser	Tyr	Met	Cys	Gln	
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	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Asp	Asn	Lys	His	Asp	Cys	Lys	Glu	
		1770					1775				1780					1785	
	GCT	GAG	TGT	GAA	CAG	AAG	ATC	CAC	AGT	CCA	AGT	GGC	CTC	ATC	ACC	AGT	3008
	Ala	Glu	Cys	Glu	Gln	Lys	Ile	His	Ser	Pro	Ser	Gly	Leu	Ile	Thr	Ser	
				1790							1795				1800		
35	CCC	AAC	TGG	CCA	GAC	AAG	TAC	CCA	AGC	AGG	AAA	GAA	TGC	ACT	TGG	GAA	3056
	Pro	Asn	Trp	Pro	Asp	Lys	Tyr	Pro	Ser	Arg	Lys	Glu	Cys	Thr	Trp	Glu	
				1805						1810					1815		
	ATC	AGC	GCC	ACT	CCC	GGC	CAC	CGA	ATC	AAA	TTA	GCC	TTT	AGT	GAA	TTT	3104
	Ile	Ser	Ala	Thr	Pro	Gly	His	Arg	Ile	Lys	Leu	Ala	Phe	Ser	Glu	Phe	
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	Glu	Ile	Glu	Gln	His	Gln	Glu	Cys	Ala	Tyr	Asp	His	Leu	Glu	Val	Phe	
				1835					1840					1845			
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45	Asp	Gly	Glu	Thr	Glu	Lys	Ser	Pro	Ile	Leu	Gly	Arg	Leu	Cys	Gly	Asn	
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	AAG	ATA	CCA	GAT	CCC	CTT	GTG	GCT	ACT	GGA	AAT	AAA	ATG	TTT	GTT	CGG	3248
	Lys	Ile	Pro	Asp	Pro	Leu	Val	Ala	Thr	Gly	Asn	Lys	Met	Phe	Val	Arg	
				1870							1875				1880		
50	TTT	GTT	TCT	GAT	GCA	TCT	GTT	CAA	AGA	AAA	GGC	TTT	CAA	GCC	ACA	CAT	3296
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				1885						1890					1895		

TCT ACA GAG TGT GGC GGA CGA TTG AAA GCA GAA TCA AAA CCA AGA GAT 3344
 Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala Glu Ser Lys Pro Arg Asp
 1900 1905 1910

CTG TAC TCA CAT GCT CAG TTT GGT GAT AAC AAC TAC CCA GGA CAG GTT 3392
 Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro Gly Gln Val
 1915 1920 1925

GAC TGT GAA TGG CTA TTA GTA TCA GAA CGG GGC TCT CGA CTT GAA TTA 3440
 Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg Leu Glu Leu
 1930 1935 1940 1945

TCC TTC CAG ACA TTT GAA GTG GAG GAA GAA GCA GAC TGT GGC TAT GAC 3488
 Ser Phe Gln Thr Phe Glu Val Glu Glu Glu Ala Asp Cys Gly Tyr Asp
 1950 1955 1960

TAT GTG GAG CTC TTT GAT GGT CTT GAT TCA ACA GCT GTG GGG CTT GGT 3536
 Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val Gly Leu Gly
 1965 1970 1975

CGA TTC TGT GGA TCC GGG CCA CCA GAA GAG ATT TAT TCA ATT GGA GAT 3584
 Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser Ile Gly Asp
 1980 1985 1990

TCA GTT TTA ATT CAT TTC CAC ACT GAT GAC ACA ATC AAC AAG AAG GGA 3632
 Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn Lys Lys Gly
 1995 2000 2005

TTT CAT ATA AGA TAC AAA AGC ATA AGA TAT CCA GAT ACC ACA CAT ACC 3680
 Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr
 2010 2015 2020 2025

AAA AAA TAA CACCAAAACC TCTGTCAGAA CACAAAGGAA TGTGCATAAT 3729
 Lys Lys *

GGAGAGAAGA CATATTTTTT TTAAAACTGA AGATATTGGC ACAAATGTTT TATACAAAGA 3789

GTTTGAACAA AAAATCCCTG TAAGACCAGA ATTATCTTTG TACTAAAAGA GAAGTTTCCA 3849

GCAAAACCCCT CATCAGCATT ACAAGGATAT TTGAACTCCA TGCTTGATGG TATTAATAAA 3909

GCTGGTGAAA 3919

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Ser Gly Ile Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly Leu Asp
 20 25 30

Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Thr Ile
 35 40 45

Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala
 50 55 60

Leu 65	Asp	Asp	Glu	Asp	Leu 70	Asn	Ile	Phe	Gln	Ile 75	Asp	Arg	Thr	Ile	Asp 80
Leu	Thr	Gln	Asn	Pro 85	Phe	Gly	Asn	Leu	Gly 90	His	Thr	Thr	Gly	Gly 95	Leu
Gly	Asp	His	Ala 100	Met	Ser	Lys	Lys	Arg 105	Gly	Ala	Leu	Tyr	Gln 110	Leu	Ile
Asp	Arg	Ile 115	Arg	Arg	Ile	Gly	Phe 120	Gly	Leu	Glu	Gln	Asn 125	Asn	Thr	Val
Lys	Gly 130	Lys	Val	Pro	Leu	Gln 135	Phe	Ser	Gly	Gln	Asn 140	Glu	Lys	Asn	Arg
Val 145	Pro	Arg	Ala	Ala	Thr 150	Ser	Arg	Thr	Glu	Arg 155	Ile	Trp	Pro	Gly	Gly 160
Val	Ile	Pro	Tyr	Val 165	Ile	Gly	Gly	Asn	Phe 170	Thr	Gly	Ser	Gln	Arg 175	Ala
Met	Phe	Lys	Gln 180	Ala	Met	Arg	His	Trp 185	Glu	Lys	His	Thr	Cys 190	Val	Thr
Phe	Ile	Glu 195	Arg	Ser	Asp	Glu	Glu 200	Ser	Tyr	Ile	Val	Phe 205	Thr	Tyr	Arg
Pro	Cys 210	Gly	Cys	Cys	Ser	Tyr 215	Val	Gly	Arg	Arg	Gly 220	Asn	Gly	Pro	Gln
Ala 225	Ile	Ser	Ile	Gly	Lys 230	Asn	Cys	Asp	Lys	Phe 235	Gly	Ile	Val	Val	His 240
Glu	Leu	Gly	His	Val 245	Ile	Gly	Phe	Trp	His 250	Glu	His	Thr	Arg	Pro 255	Asp
Arg	Asp	Asn	His 260	Val	Thr	Ile	Ile	Arg 265	Glu	Asn	Ile	Gln	Pro 270	Gly	Gln
Glu	Tyr	Asn 275	Phe	Leu	Lys	Met	Glu 280	Pro	Gly	Glu	Val	Asn 285	Ser	Leu	Gly
Glu	Arg 290	Tyr	Asp	Phe	Asp	Ser 295	Ile	Met	His	Tyr	Ala 300	Arg	Asn	Thr	Phe
Ser 305	Arg	Gly	Met	Phe	Leu 310	Asp	Thr	Ile	Leu	Pro 315	Ser	Arg	Asp	Asp	Asn 320
Gly	Ile	Arg	Pro	Ala 325	Ile	Gly	Gln	Arg	Thr 330	Arg	Leu	Ser	Lys	Gly 335	Asp
Ile	Ala	Gln	Ala 340	Arg	Lys	Leu	Tyr	Arg 345	Cys	Pro	Ala	Cys	Gly 350	Glu	Thr
Leu	Gln	Glu 355	Ser	Asn	Gly	Asn	Leu 360	Ser	Ser	Pro	Gly	Phe 365	Pro	Asn	Gly
Tyr	Pro 370	Ser	Tyr	Thr	His	Cys 375	Ile	Trp	Arg	Val	Ser 380	Val	Thr	Pro	Gly
Glu 385	Lys	Ile	Val	Leu	Asn 390	Phe	Thr	Thr	Met	Asp 395	Leu	Tyr	Lys	Ser	Ser 400
Leu	Cys	Trp	Tyr	Asp 405	Tyr	Ile	Glu	Val	Arg 410	Asp	Gly	Tyr	Trp	Arg 415	Lys

FOR 220 " 9824654

Ser Pro Leu Leu Gly Arg Phe Cys Gly Asp Lys Leu Pro Glu Val Leu
420 425 430

Thr Ser Thr Asp Ser Arg Met Trp Ile Glu Phe Arg Ser Ser Ser Asn
435 440 445

5 Trp Val Gly Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile Cys Gly Gly
450 455 460

Glu Ile Arg Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn Tyr Pro Asp
465 470 475 480

10 Asp Tyr Arg Pro Met Lys Glu Cys Val Trp Lys Ile Thr Val Ser Glu
485 490 495

Ser Tyr His Val Gly Leu Thr Phe Gln Ser Phe Glu Ile Glu Arg His
500 505 510

Asp Asn Cys Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly Thr Ser Glu
515 520 525

5 Asn Ser Pro Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys Pro Glu Asp
530 535 540

Ile Arg Ser Thr Ser Asn Thr Leu Trp Met Lys Phe Val Ser Asp Gly
545 550 555 560

Thr Val Asn Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys Glu Glu Asp
565 570 575

Glu Cys Ala Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg Cys Leu Asn
580 585 590

Thr Leu Gly Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr Glu Leu Gly
595 600 605

5 Pro Asp Arg Arg Ser Cys Glu Ala Ala Cys Gly Gly Leu Leu Thr Lys
610 615 620

Leu Asn Gly Thr Ile Thr Thr Pro Gly Trp Pro Lys Glu Tyr Pro Pro
625 630 635 640

30 Asn Lys Asn Cys Val Trp Gln Val Val Ala Pro Thr Gln Tyr Arg Ile
645 650 655

Ser Val Lys Phe Glu Phe Phe Glu Leu Glu Gly Asn Glu Val Cys Lys
660 665 670

Tyr Asp Tyr Val Glu Ile Trp Ser Gly Leu Ser Ser Glu Ser Lys Leu
675 680 685

35 His Gly Lys Phe Cys Gly Ala Glu Val Pro Glu Val Ile Thr Ser Gln
690 695 700

Phe Asn Asn Met Arg Ile Glu Phe Lys Ser Asp Asn Thr Val Ser Lys
705 710 715 720

40 Lys Gly Phe Lys Ala His Phe Phe Ser Asp Lys Asp Glu Cys Ser Lys
725 730 735

Asp Asn Gly Gly Cys Gln His Glu Cys Val Asn Thr Met Gly Ser Tyr
740 745 750

Met Cys Gln Cys Arg Asn Gly Phe Val Leu His Asp Asn Lys His Asp
755 760 765

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Cys Lys Glu Ala Glu Cys Glu Gln Lys Ile His Ser Pro Ser Gly Leu
770 775 780

Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg Lys Glu Cys
785 790 795 800

5 Thr Trp Glu Ile Ser Ala Thr Pro Gly His Arg Ile Lys Leu Ala Phe
805 810 815

Ser Glu Phe Glu Ile Glu Gln His Gln Glu Cys Ala Tyr Asp His Leu
820 825 830

10 Glu Val Phe Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu Gly Arg Leu
835 840 845

Cys Gly Asn Lys Ile Pro Asp Pro Leu Val Ala Thr Gly Asn Lys Met
850 855 860

Phe Val Arg Phe Val Ser Asp Ala Ser Val Gln Arg Lys Gly Phe Gln
865 870 875 880

15 Ala Thr His Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala Glu Ser Lys
885 890 895

Pro Arg Asp Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro
900 905 910

Gly Gln Val Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg
915 920 925

Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Glu Ala Asp Cys
930 935 940

Gly Tyr Asp Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val
945 950 955 960

20 Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser
965 970 975

Ile Gly Asp Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn
980 985 990

30 Lys Lys Gly Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr
995 1000 1005

Thr His Thr Lys Lys *
1010

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCAGCTTAAC CTGTTACAC

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACCTCTACTT CCACTTCATC

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGAACAGA AAGGAATGTG

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACCACTATT CCACATCACC

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTTGCAAGTC AGTTGCTTTG CTGG

24

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAGTGCGGCC GCACATTCCT TTGTGTTC

28

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Glu Thr Met His Ala
1 5 10 15
Lys Asn

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr
1 5 10 15
Lys Lys